



SEQUENCE LISTING

<110> Schwab, M.
Chen, M.

<120> NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO
GENES AND METHODS BASED THEREON

<130> 10200-003-999

<140> 09/830,972
<141> 2001-09-24

<150> PCT/US99/26160
<151> 1999-11-05

<150> 60/107,446
<151> 1998-11-06

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Ala Ala Gly Leu Ser Ala Ala Val Pro Pro Ala Ala Ala Ala Pro	
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ctg ccg gcc gcg ccc cct gcc gct cct gag agg cag cca tcc tgg gaa Leu Pro Ala Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu 95 100 105	579
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tca gaa atg gga tca tct ttt aaa ggc tcc cca aaa gga gag tca gcc Ser Glu Met Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala 290 295 300	1155
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gat att gtt atg gaa gca cca tta aat tct ctc ctt cca agc gct ggt Asp Ile Val Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly 590 595 600 605	2067
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cct tat ata tcc att gcg tgt gat tta att aaa gaa aca aag ctc tcc Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser 670 675 680 685	2307
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gaa tct gaa cca gtt gac tta ttt agt gat gat tcg att cct gaa gtc Glu Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val 720 725 730	2451
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770	775	780	
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Leu His Ser Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr			
785	790	795	
aaa aag gag aaa att tct ttg caa atg gaa gag ttt aat act gca att			2691
Lys Lys Glu Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile			
800	805	810	
tat tca aat gat gac tta ctt tct tct aag gaa gac aaa ata aaa gaa			2739
Tyr Ser Asn Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu			
815	820	825	
agt gaa aca ttt tca gat tca tct ccg att gag ata ata gat gaa ttt			2787
Ser Glu Thr Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe			
830	835	840	845
ccc acg ttt gtc agt gct aaa gat gat tct cct aaa tta gcc aag gag			2835
Pro Thr Phe Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu			
850	855	860	
tac act gat cta gaa gta tcc gac aaa agt gaa att gct aat atc caa			2883
Tyr Thr Asp Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln			
865	870	875	
agc ggg gca gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct			2931
Ser Gly Ala Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser			
880	885	890	
ttc aag aat ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc			2979
Phe Lys Asn Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe			
895	900	905	
tcc gaa aat agg tcc agt gta tct aag gca tcc ata tcg cct tca aat			3027
Ser Glu Asn Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn			
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gtc tct gct ttg gaa cct cag aca gaa atg ggc agc ata gtt aaa tcc			3075
Val Ser Ala Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser			
930	935	940	
aaa tca ctt acg aaa gaa gca gag aaa aaa ctt cct tct gac aca gag			3123
Lys Ser Leu Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu			
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aaa gag gac aga tcc ctg tca gct gta ttg tca gca gag ctg agt aaa			3171
Lys Glu Asp Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys			
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Thr Ser Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly			
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Val Val Phe Gly Ala Ser Leu Phe Leu Leu Ser Leu Thr Val Phe			

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Glu Asp Glu Glu Asp Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp				
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Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly				
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65 70 75 80
Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
85 90 95
Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro
100 105 110
Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Val Leu Pro Ser
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Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro
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Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr
145 150 155 160
Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu
165 170 175
Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu
180 185 190
Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly
195 200 205
Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro
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Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu
225 230 235 240
Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr
245 250 255
Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe
260 265 270
Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met
275 280 285
Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val
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Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp
305 310 315 320
Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly
325 330 335
Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn
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Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp
355 360 365
Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly
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Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp
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Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro
420 425 430
Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser
435 440 445
Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His
450 455 460
Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala
465 470 475 480
Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu
485 490 495
Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu
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Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr

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Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp	Leu Val Gln Thr Ser	
545	550	555
Glu Ala Ile Gln Glu Ser Leu Tyr Pro	Thr Ala Gln Leu Cys Pro Ser	560
565	570	575
Phe Glu Glu Ala Glu Ala Thr Pro Ser	Pro Val Leu Pro Asp Ile Val	
580	585	590
Met Glu Ala Pro Leu Asn Ser	Leu Pro Ser Ala Gly Ala Ser Val	
595	600	605
Val Gln Pro Ser Val Ser Pro	Leu Glu Ala Pro Pro Val Ser Tyr	
610	615	620
Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro	Pro Pro Tyr Glu Glu Ala	
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Met Asn Val Ala Leu Lys Ala Leu Gly	Thr Lys Glu Gly Ile Lys Glu	
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Pro Glu Ser Phe Asn Ala Ala Val	Gln Glu Thr Glu Ala Pro Tyr Ile	
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Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys	Leu Ser Thr Glu Pro	
675	680	685
Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala	Lys Phe Glu Lys Ser	
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Val Pro Glu His Ala Glu Leu Val Glu Asp	Ser Ser Pro Glu Ser Glu	
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Pro Val Asp Leu Phe Ser Asp Asp Ser	Ile Pro Glu Val Pro Gln Thr	
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Gln Glu Ala Val Met Leu Met Lys Glu Ser	Leu Thr Glu Val Ser	
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Glu Thr Val Ala Gln His Lys Glu Glu Arg	Leu Ser Ala Ser Pro Gln	
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Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe	Gln Pro Asn Leu His Ser	
770	775	780
Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro	Thr Leu Thr Lys Lys Glu	
785	790	795
Lys Ile Ser Leu Gln Met Glu Glu Phe Asn	Thr Ala Ile Tyr Ser Asn	
805	810	815
Asp Asp Leu Leu Ser Ser Lys Glu Asp	Lys Ile Lys Glu Ser Glu Thr	
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Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp	Glu Phe Pro Thr Phe	
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Val Ser Ala Lys Asp Asp Ser Pro	Lys Leu Ala Lys Glu Tyr Thr Asp	
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885	890	895
Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp	Glu Phe Ser Glu Asn	
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Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro	Ser Asn Val Ser Ala	
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Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp	Thr Glu Lys Glu Asp	
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Arg Ser Leu Ser Ala Val Leu Ser Ala Glu	Leu Ser Lys Thr Ser Val	960
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Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val
995 1000 1005
Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Ser Val Thr Ile Ser
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Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala
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Ser Ile Pro Val Ile Tyr Glu Arg His Gln Val Gln Ile Asp His Tyr
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1155 1160

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Glu Ile Ala Glu Ile Gln Asp Gly Glu Ser Leu
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1 5 10

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1 5 10 15
Ser Phe Leu Leu Leu Phe Ser Leu Thr Gln Phe Ser Val Val Ser
20 25 30
Val Val Ala Tyr Leu Ala Leu Ala Leu Ser Ala Thr Ile Ser Phe
35 40 45
Arg Ile Tyr Lys Ser Val Leu Gln Ala Val Gln Lys Thr Asp Glu Gly
50 55 60
His Pro Phe Lys Ala Tyr Leu Glu Leu Glu Ile Thr Leu Ser Gln Glu
65 70 75 80
Gln Ile Gln Lys Tyr Thr Asp Cys Leu Gln Phe Tyr Val Asn Ser Thr
85 90 95
Leu Lys Glu Leu Arg Arg Leu Phe Leu Val Gln Asp Leu Val Asp Ser
100 105 110
Leu Lys Phe Ala Val Leu Met Trp Leu Leu Thr Tyr Val Gly Ala Leu
115 120 125
Phe Asn Gly Leu Thr Leu Leu Met Ala Val Val Ser Met Phe Thr
130 135 140
Leu Pro Val Val Tyr Val Lys His Gln Ala Gln Ile Asp Gln Tyr Leu
145 150 155 160
Gly Leu Val Arg Thr His Ile Asn Ala Val Val Ala Lys Ile Gln Ala
165 170 175
Lys Ile Pro Gly Ala Lys Arg His Ala Glu
180 185

<210> 22
<211> 186
<212> PRT
<213> Rattus sp.

<400> 22

Asp	Leu	Leu	Tyr	Trp	Arg	Asp	Ile	Lys	Gln	Thr	Gly	Ile	Val	Phe	Gly
1				5				10						15	
Ser	Phe	Leu	Leu	Leu	Phe	Ser	Leu	Thr	Gln	Phe	Ser	Val	Val	Ser	
				20				25					30		
Val	Val	Ala	Tyr	Leu	Ala	Leu	Ala	Leu	Ser	Ala	Thr	Ile	Ser	Phe	
				35				40				45			
Arg	Ile	Tyr	Lys	Ser	Val	Leu	Gln	Ala	Val	Gln	Lys	Thr	Asp	Glu	Gly
				50				55			60				
His	Pro	Phe	Lys	Ala	Tyr	Leu	Glu	Leu	Glu	Ile	Thr	Leu	Ser	Gln	Glu
				65				70			75			80	
Gln	Ile	Gln	Lys	Tyr	Thr	Asp	Cys	Leu	Gln	Leu	Tyr	Val	Asn	Ser	Thr
				85				90					95		
Leu	Lys	Glu	Leu	Arg	Arg	Leu	Phe	Leu	Val	Gln	Asp	Leu	Val	Asp	Ser
				100				105					110		
Leu	Lys	Phe	Ala	Val	Leu	Met	Trp	Leu	Leu	Thr	Tyr	Val	Gly	Ala	Leu
				115				120					125		
Phe	Asn	Gly	Leu	Thr	Leu	Leu	Met	Ala	Val	Val	Ser	Met	Phe	Thr	
				130				135			140				
Leu	Pro	Val	Val	Tyr	Val	Lys	His	Gln	Ala	Gln	Val	Asp	Gln	Tyr	Leu
				145				150			155			160	
Gly	Leu	Val	Arg	Thr	His	Ile	Asn	Thr	Val	Val	Ala	Lys	Ile	Gln	Ala
				165				170					175		
Lys	Ile	Pro	Gly	Ala	Lys	Arg	His	Ala	Glu						
				180				185							

<210> 23

<211> 186

<212> PRT

<213> Gallus gallus

<400> 23

Asn	Leu	Leu	Tyr	Trp	Arg	Asp	Ile	Lys	Gln	Thr	Gly	Ile	Val	Phe	Gly
1				5					10					15	
Ser	Leu	Leu	Leu	Leu	Leu	Phe	Ser	Leu	Thr	Gln	Phe	Ser	Val	Val	Ser
						20			25				30		
Val	Val	Ala	Tyr	Leu	Ala	Leu	Ala	Gly	Leu	Ser	Ala	Thr	Ile	Ser	Phe
							35		40			45			
Arg	Ile	Tyr	Lys	Ser	Val	Leu	Gln	Ala	Val	Gln	Lys	Thr	Asp	Glu	Gly
						50			55		60				
His	Pro	Phe	Lys	Ala	Tyr	Leu	Asp	Met	Glu	Met	Asn	Leu	Ser	Gln	Asp
						65		70		75			80		
Gln	Ile	Gln	Lys	Tyr	Thr	Asp	Cys	Leu	Gln	Leu	Tyr	Val	Asn	Ser	Thr
							85			90			95		
Val	Lys	Glu	Leu	Arg	Arg	Leu	Phe	Leu	Val	Gln	Asp	Leu	Val	Asp	Ser
							100		105			110			
Leu	Lys	Phe	Ala	Val	Leu	Met	Trp	Leu	Leu	Thr	Tyr	Val	Gly	Ala	Leu
						115			120			125			
Phe	Asn	Gly	Leu	Thr	Leu	Leu	Ile	Met	Ala	Val	Val	Ser	Met	Phe	Thr
							130		135		140				
Leu	Pro	Val	Val	Tyr	Asp	Lys	Tyr	Gln	Ala	Gln	Ile	Asp	Gln	Tyr	Leu
						145			150		155			160	

Gly Leu Val Arg Thr His Ile Asn Thr Val Val Ala Lys Ile Gln Ala
165 170 175
Lys Ile Pro Gly Ala Lys Arg Lys Ala Glu
180 185

<210> 24
<211> 186
<212> PRT
<213> Bos sp.

<400> 24
Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly
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Ala Ser Leu Phe Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser
20 25 30
Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe
35 40 45
Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly
50 55 60
His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu
65 70 75 80
Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr
85 90 95
Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser
100 105 110
Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu
115 120 125
Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser
130 135 140
Val Pro Val Ile Tyr Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu
145 150 155 160
Gly Leu Ala Asn Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala
165 170 175
Lys Ile Pro Gly Leu Lys Arg Lys Ala Glu
180 185

<210> 25
<211> 186
<212> PRT
<213> Rattus sp.

<400> 25
Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly
1 5 10 15
Ala Ser Leu Phe Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser
20 25 30
Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe
35 40 45
Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly
50 55 60
His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu
65 70 75 80
Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Ser Thr
85 90 95
Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser
100 105 110
Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu

115	120	125
Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser		
130	135	140
Ile Pro Val Ile Tyr Glu Arg His Gln Val Gln Ile Asp His Tyr Leu		
145	150	155
Gly Leu Ala Asn Lys Ser Val Lys Asp Ala Met Ala Lys Ile Gln Ala		
165	170	175
Lys Ile Pro Gly Leu Lys Arg Lys Ala Asp		
180	185	

<210> 26
<211> 194
<212> PRT
<213> C. elegans

<400> 26		
Asp Val Ile Tyr Trp Arg Asp Ala Lys Lys Ser Ala Ile Val Leu Ser		
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Leu Ala Leu Leu Val Leu Phe Val Leu Ala Lys Tyr Pro Leu Leu Thr		
20	25	30
Val Val Thr Tyr Ser Leu Leu Leu Ala Leu Gly Ala Ala Gly Phe		
35	40	45
Arg Val Phe Lys Lys Val Glu Ala Gln Ile Lys Lys Thr Asp Ser Glu		
50	55	60
His Pro Phe Ser Glu Ile Leu Ala Gln Asp Leu Thr Leu Pro Gln Glu		
65	70	75
Lys Val His Ala Gln Ala Asp Val Phe Val Glu His Ala Thr Cys Ile		
85	90	95
Ala Asn Lys Leu Lys Lys Leu Val Phe Val Glu Ser Pro Leu Glu Ser		
100	105	110
Ile Lys Phe Gly Leu Val Leu Trp Ser Leu Thr Tyr Ile Ala Ser Trp		
115	120	125
Phe Ser Gly Phe Thr Leu Ala Ile Leu Gly Leu Leu Gly Val Phe Ser		
130	135	140
Val Pro Lys Val Tyr Glu Ser Asn Gln Glu Ala Ile Asp Pro His Leu		
145	150	155
Ala Thr Ile Ser Gly His Leu Lys Asn Val Gln Asn Ile Ile Asp Glu		
165	170	175
Lys Leu Pro Phe Leu Arg Ser Ala Pro Val Ala Ala Glu Glu Lys Lys		
180	185	190
Asp Gln		

<210> 27
<211> 150
<212> PRT
<213> D. melanogaster

<400> 27		
Asn Leu Leu Leu Trp Arg Asn Ser Arg Lys Thr Leu Ile Val Phe Thr		
1	5	10
Gly Ile Leu Leu Leu Leu Asp Val Met Val His Ser Val Ile Ser		
20	25	30
Val Ile Ser Met Val Gly Ile Thr Val Leu Ile Ala Ala Ile Gly His		
35	40	45
Arg Leu Leu Val Gln Phe Trp Ser Ile Trp Lys Lys Asp Glu Asn Lys		
50	55	60

Asp	Gln	Ile	Leu	Arg	Phe	Tyr	Pro	His	Pro	Lys	Ile	Glu	Ile	Pro	Arg
65	.				70					75					80
Glu	Glu	Thr	Leu	Tyr	Leu	Ala	Gly	Lys	Ala	Val	Ser	His	Ile	Asn	Leu
										85					95
Ile	Leu	Asn	Arg	Met	Ile	Glu	Leu	Leu	Ile	Val	Glu	Lys	Trp	Glu	Asp
									100		105				110
Ser	Leu	Lys	Phe	Leu	Val	Leu	Leu	Cys	Gly	Ile	Asn	Leu	Leu	Gly	Asp
								115		120					125
Cys	Phe	Asn	Gly	Leu	Thr	Leu	Leu	Ile	Phe	Gly	Met	Cys	Ile	Cys	Cys
								130		135					140
Leu	Thr	Leu	Leu	Tyr	Leu										
145										150					

<210> 28
<211> 3833
<212> DNA
<213> Bos sp.

<400> 28
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 gagaaggCAA aaaatccatt tgttagAGAGA aatttaACAG aattttcAGA attGGAATAT
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 aatccTAGGG acgAAATAGT tgtgaggAGT agagataAAAG aagaggACTT agttAGTCTT
 aacatcCTTC atactcAGCA ggagttATCT acagtCCtTA cgAAATCAGT tGAAGAAGAA
 gatAGAGTC tgTCTCCAGA aaaaacaAAAG gacAGTTTA aggAAAAGGG agttGCAGCA
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 aaagataACTT acaAGCAAGA tagtgatGTT ttgattGCTG gagGtaATAT agAGAGCaaa
 ttGGAAGGTA aagtGGATAA gaaACACtT tcAGATAGCC ttGAAcAAAC aatcGTGAA
 aaAGATAGTg aaAGCAGTAA tgatGACACT tcatttCCCA gtacACCAGA agctGTAAGA
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 tggacCTTGT tcaAAActtCA gaagctGtGc aggAGtCACT ttAccCtGtA acacAGtTT
 gcccAtCTT tgaAGAAAtCT gaagctACTC cgtcAccCGGt ttGcCtGAC attGtCatGG
 aAGCACCATT aaAttCtGtA gttCCTAGtG ctGgtGtCttC tGcAGtGcAG ctcAGtTCA
 caccATTAGA aactCttCCtC tcAGtTAATT atGAAAGCAT aaAGtttGAG cctGAAAAtC
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 aAGATTCCtC ccccGATTCT gaAccAGTTG acTTAtTTAG tGAtGATTCA atACCCGAAG
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 agttCTCCAA agAtAGGGtG tGtGttCtAA agtGcccGt actGcCtCCA gatGttCtG
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 2280

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tatatagtgt	ttcacgaagc	ttagccctt	acctcccaag	ctgccccaca	gtgcttgata	3480
cttctgtcat	gggtttatg	tgtgttagtcc	caaagcacat	aagctaggga	gaaacgtact	3540
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cgatttatac	aattgtgggtt	taagctgtat	tgaactaaat	ctgtggaatg	cattgtgaac	3780
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<210> 29
<211> 1178
<212> PRT
<213> *Homo sapiens*

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<220>
<221> VARIANT
<222> (1)...(1178) at all Xaa position
<223> Xaa = any amino acid
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<400> 29

Met	Glu	Asp	Leu	Asp	Gln	Ser	Pro	Leu	Val	Ser	Ser	Ser	Asp	Ser	Pro
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Pro	Arg	Pro	Gln	Pro	Ala	Phe	Lys	Tyr	Gln	Phe	Val	Arg	Glu	Pro	Glu
					20				25					30	
Asp	Glu	Asp	Glu	Asp	Glu	Asp									
						35			40				45		
Leu	Glu	Glu	Leu	Glu	Val	Leu	Glu	Arg	Lys	Pro	Ala	Ala	Gly	Leu	Ser
						50			55			60		.	
Ala	Ala	Pro	Val	Pro	Thr	Ala	Pro	Ala	Ala	Gly	Ala	Pro	Leu	Met	Asp
					65				70			75			80
Phe	Gly	Asn	Asp	Phe	Val	Pro	Pro	Ala	Pro	Arg	Gly	Pro	Leu	Pro	Ala
						85				90				95	
Ala	Pro	Pro	Val	Ala	Pro	Glu	Arg	Gln	Pro	Ser	Trp	Asp	Pro	Ser	Pro
						100				105				110	
Val	Ser	Ser	Thr	Val	Pro	Ala	Pro	Ser	Pro	Leu	Ser	Ala	Ala	Ala	Val
						115				120				125	
Ser	Pro	Ser	Lys	Leu	Pro	Glu	Asp	Asp	Glu	Pro	Pro	Ala	Arg	Pro	Pro
						130			135			140			
Pro	Pro	Pro	Pro	Ala	Ser	Val	Ser	Pro	Gln	Ala	Glu	Pro	Val	Trp	Thr

145	150	155	160
Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro			
165	170	175	
Lys Arg Arg Gly Ser Ser Gly Ala Val Val Xaa Xaa Xaa Xaa Lys Ile			
180	185	190	
Met Asp Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu			
195	200	205	
Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Xaa Pro Ser Leu			
210	215	220	
Ser Pro Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn			
225	230	235	240
Leu Ser Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser			
245	250	255	
Glu Ala Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp			
260	265	270	
Arg Asp Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser			
275	280	285	
Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn			
290	295	300	
Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu Lys Leu			
305	310	315	320
Val Ser Asn Asn Ile Leu His Xaa Gln Gln Glu Leu Pro Thr Ala Leu			
325	330	335	
Thr Lys Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys			
340	345	350	
Asp Ser Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu			
355	360	365	
Glu Tyr Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp			
370	375	380	
Ser Lys Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser			
385	390	395	400
Asn Leu Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu			
405	410	415	
Gln Thr Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser			
420	425	430	
Phe Pro Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile			
435	440	445	
Thr Cys Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn			
450	455	460	
Ile Phe Pro Leu Leu Glu Asp Pro Thr Ser Glu Asn Xaa Thr Asp Glu			
465	470	475	480
Lys Lys Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr			
485	490	495	
Ser Thr Lys Thr Ser Asn Pro Phe Phe Val Ala Ala Gln Asp Ser Glu			
500	505	510	
Thr Asp Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val			
515	520	525	
Val Ala Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala			
530	535	540	
Cys Glu Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu			
545	550	555	560
Thr Lys Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu			
565	570	575	
Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr			
580	585	590	
Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser			
595	600	605	

Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro
610 615 620
Leu Glu Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu
625 630 635 640
Asn Pro Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Val Ser
645 650 655
Gly Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu
660 665 670
Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys
675 680 685
Glu Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser
690 695 700
Glu Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val
705 710 715 720
Glu Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp
725 730 735
Ser Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val
740 745 750
Lys Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu
755 760 765
Asn Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr
770 775 780
Leu Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu
785 790 795 800
Pro Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln
805 810 815
Met Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile
820 825 830
Ser Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser
835 840 845
Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr
850 855 860
Asp Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser
865 870 875 880
His Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro
885 890 895
Cys Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys
900 905 910
Val Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser
915 920 925
Ala Thr Ser Lys Val Leu Leu Pro Pro Asp Val Ser Ala Leu Gly
930 935 940
His Thr Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Glu
945 950 955 960
Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg
965 970 975
Ser Pro Ser Ala Ile Phe Ser Ala Asp Leu Gly Lys Thr Ser Val Val
980 985 990
Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly
995 1000 1005
Ala Ser Leu Phe Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser
1010 1015 1020
Val Thr Ala Tyr Ile Ala Leu Ala Leu Ser Val Thr Ile Ser Phe
1025 1030 1035 1040
Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly
1045 1050 1055
His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu

	1060	1065	1070
Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr			
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Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser			
1090	1095	1100	
Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu			
1105	1110	1115	1120
Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser			
1125	1130	1135	
Val Pro Val Ile Tyr Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu			
1140	1145	1150	
Gly Leu Ala Asn Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala			
1155	1160	1165	
Lys Ile Pro Gly Leu Lys Arg Lys Ala Glu			
1170	1175		

<210> 30
 <211> 1163
 <212> PRT
 <213> Homo sapiens

<220>
 <221> VARIANT
 <222> (1)...(1163) at all Xaa position
 <223> Xaa = any amino acid

	<400> 30		
Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser Thr Asp Ser			
1	5	10	15
Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro			
20	25	30	
Glu Asp Glu Glu Asp Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp			
35	40	45	
Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly			
50	55	60	
Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Pro Leu Leu Asp			
65	70	75	80
Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala			
85	90	95	
Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro			
100	105	110	
Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Val Leu Pro Ser			
115	120	125	
Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro			
130	135	140	
Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr			
145	150	155	160
Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu			
165	170	175	
Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu			
180	185	190	
Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly			
195	200	205	
Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro			
210	215	220	
Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu			
225	230	235	240

Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr
245 250 255
Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe
260 265 270
Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met
275 280 285
Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val
290 295 300
Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp
305 310 315 320
Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly
325 330 335
Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn
340 345 350
Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp
355 360 365
Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly
370 375 380
Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp
385 390 395 400
Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp
405 410 415
Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro
420 425 430
Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser
435 440 445
Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His
450 455 460
Thr Ser Glu Asn Xaa Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala
465 470 475 480
Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu
485 490 495
Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu
500 505 510
Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr
515 520 525
Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr
530 535 540
Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser
545 550 555 560
Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser
565 570 575
Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
580 585 590
Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val
595 600 605
Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
610 615 620
Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
625 630 635 640
Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu
645 650 655
Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
660 665 670
Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro
675 680 685
Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser

690	695	700
Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu		
705	710	715
Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr		
725	730	735
Gln Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser		
740	745	750
Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln		
755	760	765
Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser		
770	775	780
Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu		
785	790	795
Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn		
805	810	815
Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr		
820	825	830
Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe		
835	840	845
Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp		
850	855	860
Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala		
865	870	875
Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn		
885	890	895
Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn		
900	905	910
Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala		
915	920	925
Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu		
930	935	940
Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp		
945	950	955
Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val		
965	970	975
Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe		
980	985	990
Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val		
995	1000	1005
Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Ser Val Thr Ile Ser		
1010	1015	1020
Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu		
1025	1030	1035
Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu		
1045	1050	1055
Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Ser		
1060	1065	1070
Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp		
1075	1080	1085
Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala		
1090	1095	1100
Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe		
1105	1110	1115
Ser Ile Pro Val Ile Tyr Glu Arg His Gln Val Gln Ile Asp His Tyr		
1125	1130	1135
Leu Gly Leu Ala Asn Lys Ser Val Lys Asp Ala Met Ala Lys Ile Gln		
1140	1145	1150

Ala Lys Ile Pro Gly Leu Lys Arg Lys Ala Asp
1155 1160

<210> 31
<211> 1568
<212> DNA
<213> Rattus sp.

<400> 31

caggcttagt	ctgggaaagc	gggtgtttca	tgttcaggg	agaatttgc	agtttacagc	60
gtttctgttg	gtatgcataa	tttgaattg	ctgctggagg	gcagatctg	gcaagaaatg	120
gacggacaga	agaaacattt	gaaggacaag	gttggacc	tcctctactg	gagagacatt	180
aagaagactg	gagtgtgtt	ttgtgccagc	ttattcctgc	tgctgtctc	gacagtgttc	240
agcattgtca	gtgtaacggc	ctacattgcc	ttggccctgc	tctcggtgac	tatcagcttt	300
aggatataata	agggcgtat	ccaggctatc	cagaatcag	atgaaggcca	cccattcagg	360
gcataatttag	aatctgaagt	tgctatatca	gaggaattgg	ttcagaaata	cagtaattct	420
gctcttggtc	atgtgaacag	cacaataaaa	gaactgaggc	ggctttctt	agttgatgat	480
ttagttgatt	ccctgaagtt	tgcaagtgtt	atgtgggtgt	ttacttatgt	ttggccttg	540
ttaaatggtc	tgacactact	gattttatgt	ctgatctac	tcttcagtat	tcctgttatt	600
tatgaacacggc	atcagggtca	gatacatat	tatctaggac	ttgcaaaca	gaggttaag	660
gatgccatgg	ccaaaatcca	agaaaaatc	cctgattga	agcgc当地	agattgaaaa	720
agccccaaac	agaagttcat	ctttaaaggg	gacactca	tgattacggg	gggggaggt	780
caggggttag	cccttgggtgg	ccgtgcgggt	tcagctctt	attttagca	gtgcactgtt	840
tgaggaaaaaa	ttacctgtct	tgacttcctg	tgtttatcat	cttaagtatt	gtaagctgtct	900
gtgtatggat	ctcatgttag	tcacacttgt	cttcccaat	gaggcgcctg	gtgatataaag	960
gactcgggga	aagctgtca	ttgtatctgc	tgcaggtag	tctagctgt	tgcagagat	1020
tgtaaagaag	gcaaatctgg	gggcagggaa	aaccctttc	acagtgtact	gtgtttggtc	1080
agtgtaaaac	tgtatcgat	ttttctgaaa	tgaaatgtt	agatgagagc	atactactaa	1140
accagagtgg	aaaactctgt	ctttatggtg	tgttctaggt	gtattgtgaa	tttactgtta	1200
tattgccaat	ataagtaaat	atagaccta	tctatata	gtgtttcaca	aagtttagat	1260
cttaaacctt	gcagctgccc	cacagtctt	gacctctgag	tcattggta	tgcagtgttag	1320
tcccaagcac	ataaaactagg	aagagaaatg	tattttagg	agtgtcacct	accacctgtt	1380
ttaaagaaaa	tatagaactc	caacaaaaat	atagaatgtc	atttcaaaga	cttactgtat	1440
gtatagttaa	ttttgtcaca	gactctgaaa	ttctatggac	tgaatttcat	gcttccaaat	1500
gtttgcagtt	atcaaacatt	gttatgcaag	aaatcataaa	atgaagactt	ataccattgt	1560
ggtttaag						1568

<210> 32

<211> 199
<212> PRT
<213> Rattus sp.

<400> 32

Met	Asp	Gly	Gln	Lys	Lys	His	Trp	Lys	Asp	Lys	Val	Val	Asp	Leu	Leu
1				5				10					15		
Tyr	Trp	Arg	Asp	Ile	Lys	Lys	Thr	Gly	Val	Val	Phe	Gly	Ala	Ser	Leu
				20				25				30			
Phe	Leu	Leu	Leu	Ser	Leu	Thr	Val	Phe	Ser	Ile	Val	Ser	Val	Thr	Ala
				35				40			45				
Tyr	Ile	Ala	Leu	Ala	Leu	Leu	Ser	Val	Thr	Ile	Ser	Phe	Arg	Ile	Tyr
				50				55			60				
Lys	Gly	Val	Ile	Gln	Ala	Ile	Gln	Lys	Ser	Asp	Glu	Gly	His	Pro	Phe
				65				70			75		80		
Arg	Ala	Tyr	Leu	Glu	Ser	Glu	Val	Ala	Ile	Ser	Glu	Glu	Leu	Val	Gln
				85				90			95				
Lys	Tyr	Ser	Asn	Ser	Ala	Leu	Gly	His	Val	Asn	Ser	Thr	Ile	Lys	Glu

100	105	110	
Leu Arg Arg Leu Phe Leu Val Asp Asp	Leu Val Asp Ser	Leu Lys Phe	
115	120	125	
Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala	Leu Phe Asn Gly		
130	135	140	
Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser	Leu Phe Ser Ile Pro Val		
145	150	155	160
Ile Tyr Glu Arg His Gln Val Gln Ile Asp His	Tyr Leu Gly Leu Ala		
165	170	175	
Asn Lys Ser Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro			
180	185	190	
Gly Leu Lys Arg Lys Ala Asp			
195			

<210> 33
 <211> 18
 <212> PRT
 <213> Bos sp.

<400> 33			
Ser Tyr Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu			
1	5	10	15
Glu Ala			

<210> 34
 <211> 13
 <212> DNA
 <213> Homo sapiens

<400> 34	
gccgcccrrcca tgg	13

<210> 35
 <211> 248
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)... (248) at all n positions
 <223> n=a, c, g or t

<400> 35	
gagccgtcac cacagtaggt ccctcggtc agtcggccca gcccctctca gtcctccccca	60
accccccacaa ccgccccgc tcctgagacg cgccccggcg gcggcggcan agctgcagca	120
tcatctccac cctccagcca tggaaagacct ggaccagtct cctctggctct cgtcctcgga	180
cagcccaccc cggccgcagc cccgcgttcaa gtaccagttc gtgaggggagc ccgaggacga	240
ggaggaag	248

<210> 36
 <211> 379
 <212> DNA
 <213> Homo sapiens

<220>

```

<221> misc_feature
<222> (1)... (36) at all n positions
<223> n=a, c, g or t

<400> 36
gaaaatatgg acttgaagga gcagccagg aacactattt cggctggtca agaggattc          60
ccatctgtcc tgcttcaaac tgctgcttct nttccttctc tgtctcctct ctcagccgct        120
tcttcaaaag aacatgaata ctttgtaat ttgtcaacag tattaccac tgaaggaaca        180
cttcaagaaa atgtcagtga agcttctaaa gaggtcttag agaaggcaaa aactctactc        240
atagatagag atttaacaga gttttcagaa ttaggaatac tcagaaatgg gatcatcggt        300
cagtgtctct cccaaagcag aatctgccgt aaatagtagg caaatcctag gggaaagaaat      360
aattcgtgga aaaataaaat                                     379

<210> 37
<211> 281
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)... (281) at all n positions
<223> n=a, c, g or t

<400> 37
gatagagatt taacagagtt ttcagaatta gaatacttag aaatgggatc atcggtcagt          60
gtctctccaa aagcagaatc tgccgtataa gtagcaaatc cttaggaaaga aataatcggt        120
aaaaataaaag atgaagaaga gaagtttagt agtaataaca tccttcataa tcaacaagag        180
ttacctacag ctcttactaa attggtaaa gaggatgaag ttgtgtcttc agaaaaagca        240
aaagacagtt ttatgaaaga gagttgcagt ggaantcctt g                                281

<210> 38
<211> 640
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)... (640) at all n positions
<223> n=a, c, g or t

<400> 38
ttaaagagga tgaagttgtg tcttcagaaaa aagcaaaaga cagtttaat gaaaagagag          60
ttgcagtggaa agctccatag agggaggaat atgcagactt caaacattt gagcgagtat        120
ggaaagtgaa agatagtaag gaagatagtg atatgttggc tgctggaggt aaaatcgaga        180
gcaacttggaa aagtaaagtg gataaaaaat gtttgcaga tagcctttag caaactaatc        240
acaaaaaaga tagtgagagt agtaatgtg atacttctt ccccagtacg ccagaaggta        300
taaaggatcg ttcaggagca tatatcacat gtgctccctt taaccagca gcaactgaga        360
gcattgcaac naacattttt cctttgtgg agatcctact tcagaaaatt agaccgtgaa       420
aaaaaaataga agaaaaagaag gccnaatgtt accgagaaga atactagcac aaanctcaac      480
cctttcttgt gcagcacagg ntctngaca gatatgtccc acgnttatttccaagtgctg        540
agantcttgc aacatcctga ngctgactcc gattgttccn gagcttggaa tggattgtgg       600
ttctggtcaa gttntttgan caaatggctt gtcactcgat                               640

<210> 39
<211> 346
<212> DNA
<213> Homo sapiens

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<220>
<221> misc_feature
<222> (1)... (346) at all n positions
<223> n=a, c, g or t

<400> 39

ctgtgcccgg ccccacccccc tggcagatg tccccactg ctaaggctgc tggctcagg	60
gagggttagc ctgcaccgcgc gccaccctgc ccctaagtttta ttacctctcc agttcctacc	120
gtactccctg caccgtctca ctgtgtgtnt cgtgtcagta atttatatgg tgtaaaatg	180
tgtatatttt tgtatgtac tattttact agggctgagg ggcctgcgcc cagagctggc	240
ctcccncncaac acctgtcgctg cttggtaggt gtgggtggcgt tatggcagcc cggctgctgc	300
ttggatgcga gnttgnctt gggccgggtgc tggggggcac agttgt	346

<210> 40

<211> 325
<212> DNA
<213> Homo sapiens

<400> 40

gtggcaaaca tgcctgaagg cctgactcca gatttagtac aggaagcatg taaaagtga	60
ttgaatgaag ttactggtaaaagattgtcttatgaaacaa aatggacttg gttcaaacat	120
cagaagttat gcaagagtca ctctatcctg cagcacagct ttgcccattca tttgaagagt	180
cagaagctac tccttcacca gttttgcctg acattgttat ggaagcacca ttgaattctg	240
cagttcctag tgctgggtct tccgtgatac agcccgagctc atcaccattta gaggcttctt	300
cagttaattttt tgaagcataaa acatg	325

<210> 41

<211> 338
<212> DNA
<213> Homo sapiens

<400> 41

gcatgtgaaa gtatgttact ggtacaaaga ttgcttatga aaaaaaatg	60
gacttgggttc aaacatcaga agttatgcaa gagtcactct atcctgcagc acagcttgc	120
ccatcatttt aagagtcaga agctactcct tcaccagttt tgccctgacat tgttatggaa	180
gcaccattga attctgcagt tccttagtgc ggtgcttccg tgatacagcc cagctcatca	240
ccatttagaaatgttccatgt taattatgaa agcataaaac atgagcctga aaacccccc	300
ccatcatgaaaggccatgatgtatcacta aaaaaagt	338

<210> 42

<211> 480
<212> DNA
<213> Homo sapiens

<220>

<221> misc_feature
<222> (1)... (480) at all n positions
<223> n=a, c, g or t

<400> 42

aagactggag tgggtttgg tgccagccta ttccctgctgc tttcatttgc agtattcagc	60
attgtgagcg taacagccta cattgccttgc gcctgtct ctgtgaccat cagctttagg	120
atatacaagg gtgtgatcca agctatccag aaatcagatg aaggccaccc attcaggggca	180
tatctggaaat ctgaagttgc tataatctgag gagttgggtc agaagtacag taattctgct	240
cttggcatg tgaactgcac gataaaggaa ctcaggcgcc tcttcttagt tgatgattta	300
gttgattctc tgaagttgc agtggatgtatc tctatgttgg tgccttgg	360

aatggtctga cactactgat ttnggctctc attccactcc tncaagtgtt cctggattt 420
ntgaacggca tcnggcacag ntagatcatt atccaggact tgcaaataagg aatgtaaaga 480

<210> 43
<211> 13
<212> PRT
<213> Homo sapiens

<400> 43

Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser
1 5 10

<210> 44
<211> 16
<212> PRT
<213> Homo sapiens

<400> 44

Lys Ile Met Asp Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly
1 5 10 15

<210> 45
<211> 19
<212> PRT
<213> Homo sapiens

<400> 45

Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser Phe Asn
1 5 10 15

Glu Lys Arg

<210> 46
<211> 50
<212> PRT
<213> Homo sapiens

<400> 46

Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu
1 5 10 15

Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala
20 25 30

Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln Pro
35 40 45

Ser Ser
50

<210> 47
<211> 26
<212> DNA
<213> Artificial Sequence

<220>

<223> degenerate oligonucleotides designed from the bovine NI220
peptide 1 sequence

<220>

<221> modified base
<222> (1)... (26) at all n positions
<223> n=inosine

<400> 47
tcngtnggya anacngcngg yaartc 26

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate oligonucleotides designed from the bovine NI220 peptide 1 sequence

<220>
<221> modified_base
<222> (1)... (23) at all n positions
<223> n=inosine

<400> 48
tcngtnggna gnacnrgyaa ytc 23

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate oligonucleotides designed from the bovine NI220 peptide 1 sequence

<220>
<221> modified_base
<222> (1)... (25) at all n positions
<223> n=inosine

<400> 49
tcngtnggya anacngcggg agrtc 25

<210> 50
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate oligonucleotides designed from the bovine NI220 peptide 1 sequence

<220>
<221> modified_base
<222> (1)...(26) at all n positions
<223> n=inosine

<400> 50
tcngtnggna gnacngcngg nagrtc 26

<210> 51
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate oligonucleotides designed from the bovine NI220 peptide 2 sequence

<220>
<221> modified_base
<222> (1)... (26) at all n positions
<223> n=inosine

<400> 51
garathgcng anathcarga yggnga

26